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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 19:42:15 : search time 2002.99 seconds
(without alignments)
8149.166 Million cell updates/sec

Title: US-09-597-771-11
Perfect score: 780
Sequence: 1 aaagaatcttaga~~g~~agaaaa... gcaaaaaaaaaaaaaaaa 780

Scoring table: IDENTITY_NUC
GapOp 10.0 , GapExt 1.0

Searched: 179656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : GenBank:
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_on:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_to:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vl:*
 15: em_bb:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_ml:*
 20: em_on:*
 21: em_or:*
 22: em_ox:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_vl:*
 29: em_vn:*
 30: em_hhg_hun:*
 31: em_hhg_inv:*
 32: em_hrg_other:*
 33: em_hrg_inv:*

ALIGMENTS

RESULT 1

RESULT	1	LOCUS	AX068851	DEFINITION	Sequence 11 from Patent WO0102592.	DNA	linear	PAT	25-JAN-2001
ACCESSION	AX068851	VERSION	AX068851.1	KEYWORDS	tomato.				
ORGANISM	Lycopersicon esculentum				Eukaryota; Vidiplanteae; Streptophyta; Embryophyta; Tracheophyta; Lycopersicon.				
REFERENCE	1 (bases 1 to 780)	AUTHORS	Thompson,J.E., Wang,T.W. and Lu,D.L.	TITLE	Dna encoding a plant deoxyhypusine synthase, a plant eukaryotic initiation factor 5a, transgenic plants and a method for controlling senescence and programmed cell death in plants				
JOURNAL	Senesco, Inc. (US)	FEATURES	I. 780	source	/organism="Lycopersicon esculentum"				

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BASE COUNT	253	a	141	c	171	g	215	t
ORIGIN	"SLTESGNKDDRLPIDENLLQVKGQEGKLIVVSMSAMGEEQINAVKDGVKN							
Query Match 100.0%; Score 780; DB 6; Length 780; Best Local Similarity 100.0%; Pred. No. 1. 3e-183; Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
REFERENCE	1 (bases 1 to 779) Isolation and Characterization of Senescence-induced cDNAs Encoding Deoxyhypusine Synthase and Eukaryotic Translation Initiation Factor 5A from Tomato Wang, T.-W., Lu, L., Wang, D., and Thompson, J.E.							
ACCESSION	AF296084							
DEFINITION	Lycopersicon esculentum eukaryotic translation initiation factor 5A-2 mRNA, complete cds.							
VERSION	AF296084.1							
KEWORDS	ATP-binding; ATPase; CTD; Eukaryotic; Initiation; mRNA; Protein; RNA; Subunit; Translation							
SOURCE	Organism: <i>Lycopersicon esculentum</i> ; Kingdom: Eukarya; Phylum: Plantae; Class: Asteridae; Order: Solanales; Family: Solanaceae; Genus: <i>Solanum</i> ; Species: <i>Solanum lycopersicum</i> . Author: euansteroids I; Email: euansteroids@users.sourceforge.net							
ORGANISM	Lycopersicon esculentum Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Angiosperms; Rosids; Asterids; Solanales; Solanaceae; Solanum; Lycopersicon.							
AUTHORS	Wang, T.-W., Lu, L., Wang, D., and Thompson, J.E.							
JOURNAL	J. Biol. Chem. 276 (20), 17541-17549 (2001)							
PUBLMED	11278418							
REFERENCE	2 (bases 1 to 779) Wang, T.-W., Wang, D., Lu, L., and Thompson, J.E.							
AUTHORS	Wang, T.-W., Wang, D., Lu, L., and Thompson, J.E.							
TITLE	Direct Submission (16-Aug-2000) Biology, University of Waterloo, Waterloo, ON N2L 3G1, Canada							
JOURNAL	Biology, University of Waterloo, Waterloo, ON N2L 3G1, Canada							
FEATURES	Location/Qualifiers 1. .779 /organism="Lycopersicon esculentum" /db_xref="taxon:4081" /note="elf-5A2" /codon_start=1 /product="eukaryotic translation initiation factor 5A-2" /protein_id="P453648_1" /protein_start="12578755" /translation="MSDEEHFESKADAGASKTFPOQACTIRKNGYIVKGRCKVVE VPSKTGHGHAKCHKCVHIDFNGKLEIDPVSSPHNRYDOLIDSEDFV SLLTESGNKDDRLPIDENLLQVKGQEGKLIVVSMSAMGEEQINAVKDGVKN							
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BASE COUNT	251	a	141	c	171	g	216	t
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Query Match	98.1%; Score 765; DB 8; Length 779; Best Local Similarity 99.7%; Pred. No. 7. 2e-180; Matches 777; Conservative 0; Mismatches 2; Indels 1; Gaps 1;							
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Db	411	TGAAATCCTTCACTGATCAAAGGACGGTTGCCAGGAAAGACTGGAAAGATCATCTCCGGTCTCCACAA	281
LOCUS	AB004825	726 bp mRNA linear PLN 05-FEB-1999	
DEFINITION	Solanum tuberosum mRNA for eukaryotic initiation factor 5A4, complete cds.		
ACCESSION	AB004825		
VERSION	AB004825.1	GI:2225882	
KEYWORDS	eukaryotic initiation factor 5A4.		
SOURCE	Solanum tuberosum (cultivar: Irish Cobbler) developing microtuber microtuber cDNA to mRNA.		
ORGANISM	Solanum tuberosum		
REFERENCE	In, J.G.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (13-JUN-1997) Jun Gyo In, Hokkaido University, Faculty of Agriculture, Department of Botany; Kita 9 Nishi 9, Kita-ku, Sapporo, Hokkaido 060, Japan (E-mail: in@2.hines.hokudai.ac.jp), Tel:+81-11-706-2482, Fax:+81-11-706-2471		
REFERENCE	In, J.G., Fujino, K. and Kikuta, Y.		
AUTHORS	Nucleotide sequence of five cDNAs (accession Nos. AB004823-AB004827) encoding eukaryotic translation initiation factor 5A (eIF-5A) from potato (PGR97-147)		
JOURNAL	Plant Physiol. 115: 864 (1997)		
FEATURES	Location/Qualifiers		
Source	1. .726 /organism="Solanum tuberosum" /cultivar="Irish Cobbler" /db_xref="taxon:4113" /feature_type="microtuber" /codon_start=1 /product="eukaryotic initiation factor 5A4" /gene="eIF5A4" /genotype="eIF5A4"		
CDS	44. .523 /gene="eIF5A4" /codon_start=1 /product="eukaryotic initiation factor 5A4" /db_xref="taxon:1225883" /translation="MSDEPHQSKADAGASKTYPOQAGTIRKSGYIVIKGRCKVVEVSTSKKGKHHAKCHFVAIDIFFGKLELDIVPPSHNCVPHNRKDQLIDSEDGVSLUDNGNPKDDLULPTDSLQIKDFAEGKDLVVSMSAMGEEQINALKDIGPK"		
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Query Match	42.1%	Score 328 4; DB 8; Length 726;	
Best Local Similarity	80.1%	Pred. No. 2.8e-71;	
Matches	3865	Conservative 0; Mismatches 95; Index 0; Gaps 0;	
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Qy	102	cccaccaactggaccacccaaactggaaacacggaaatgtcaaggccgtccctg 161	
Db	103	CCCTCAACAAAGCTGGTACTATGTAGAGCGGTATCATGTCACAAAGGCCCTCATG 162	
Qy	162	caagggtgttgcgttcaettcaaactggaaacacggaaatgtcaaggccgtccctg 221	
Db	163	CAGGTGTGAGCTACATCCAACCTGGCAGCAGTGATGCCAACATGAT 222	
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VERSION			
KEYWORDS			
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ORGANISM			
REFERENCE			
AUTHORS			
JOURNAL			
FEATURES			
Source			
RESULT	12		
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LOCUS	AF416338	649 bp mRNA linear PLN 03-OCT-2001	
DEFINITION	Medicago sativa eukaryotic translation initiation factor 5A-2 mRNA, complete cds.		
ACCESSION	AF416338		
VERSION	AF416338.1	GI:15866586	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
JOURNAL			
FEATURES			
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RESULT	12		
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LOCUS	AF416338	649 bp mRNA linear PLN 03-OCT-2001	
DEFINITION	Medicago sativa eukaryotic translation initiation factor 5A-2 mRNA, complete cds.		
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ORGANISM			
REFERENCE			
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JOURNAL			
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		Deoxyhypusine Synthase and Eucaryotic Translation Initiation Factor					
		5A from Tomato					
		Wang, T.W., Lu, L., Wang, D. and Thompson, J.E.					
		J. Biol. Chem. 276 (20), 17541-17549 (2001)					
		REFERENCE					
		1 (bases 1 to 810)					
		JOURNAL					
		11278418					
		AUTHORS					
		2 (bases 1 to 810)					
		Direct Submission					
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